



## SEQUENCE LISTING

<110> Hofmann, Kathryn J.  
 Jansen, Kathrin U.  
 Neeper, Michael P.

<120> DNA ENCODING HUMAN PAPILLOMAVIRUS TYPE  
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 <141> 2001-09-17

<150> PCT/US96/03649  
 <151> 1996-03-18

<150> 08/408,669  
 <151> 1995-03-22

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 agattattaa ctgtgttata tccatatttt aggttccctg caggtggtgg caataaggcag 180  
 gatatttcttata aggttctgc ataccaatata agagtatttc ggggtcagtt acctgaccctt 240  
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 gaggacgtt gggacaatgt gtctgttagat tataaggcaga cacagttatg tattttggc 480  
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 aatggtatct gctggcataa tcaatttattt gttactgtgg tagataccac tcgtgttacc 1020  
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 cccttatgata agttaaagtt tggatgttgg gattttaaagg aaaaggtttc tttggactta 1380  
 gatcaatatac cccttggacg taaatttttgc gttcaggctg gattgcgtcg caagcccacc 1440  
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1524

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&lt;211&gt; 507

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; HPV18 L1 Consensus Sequence

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Ile	Phe	Tyr	His	Ala	Gly	Ser	Ser	Arg	Leu	Leu	Thr	Val	Gly	Asn	Pro
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Asn	Lys	Phe	Gly	Leu	Pro	Asp	Asn	Ser	Ile	Tyr	Asn	Pro	Glu	Thr	Gln
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Leu	Gly	Val	Gly	Leu	Ser	Gly	His	Pro	Phe	Tyr	Asn	Lys	Leu	Asp	Asp
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Thr	Glu	Ser	Ser	His	Ala	Ala	Thr	Ser	Asn	Val	Ser	Glu	Asp	Val	Arg
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Asp	Asn	Val	Ser	Val	Asp	Tyr	Lys	Gln	Thr	Gln	Leu	Cys	Ile	Leu	Gly
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Cys	Ala	Pro	Ala	Ile	Gly	Glu	His	Trp	Ala	Lys	Gly	Thr	Ala	Cys	Lys
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Ser	Arg	Pro	Leu	Ser	Gln	Gly	Asp	Cys	Pro	Pro	Leu	Glu	Leu	Lys	Asn
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Pro	Tyr	Gly	Asp	Ser	Met	Phe	Phe	Cys	Leu	Arg	Arg	Glu	Gln	Leu	Phe
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Ala	Arg	His	Phe	Trp	Asn	Arg	Ala	Gly	Thr	Met	Gly	Asp	Thr	Val	Pro
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Gln	Ser	Leu	Tyr	Ile	Lys	Gly	Thr	Gly	Met	Arg	Ala	Ser	Pro	Gly	Ser
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Cys	Val	Tyr	Ser	Pro	Ser	Pro	Ser	Gly	Ser	Ile	Val	Thr	Ser	Asp	Ser
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Gln	Leu	Phe	Asn	Lys	Pro	Tyr	Trp	Leu	His	Lys	Ala	Gln	Gly	His	Asn
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Thr	Arg	Ser	Thr	Asn	Leu	Thr	Ile	Cys	Ala	Ser	Thr	Gln	Ser	Pro	Val
										340		345			350
Pro	Gly	Gln	Tyr	Asp	Ala	Thr	Lys	Phe	Lys	Gln	Tyr	Ser	Arg	His	Val
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Glu	Glu	Tyr	Asp	Leu	Gln	Phe	Ile	Phe	Gln	Leu	Cys	Thr	Ile	Thr	Leu
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Thr	Ala	Asp	Val	Met	Ser	Tyr	Ile	His	Ser	Met	Asn	Ser	Ser	Ile	Leu
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Glu	Asp	Trp	Asn	Phe	Gly	Val	Pro	Pro	Pro	Pro	Thr	Thr	Ser	Leu	Val

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Ala Ala Pro Ala Glu Asn Lys Asp Pro Tyr Asp Lys Leu Lys Phe Trp			
435	440	445	
Asn Val Asp Leu Lys Glu Lys Phe Ser Leu Asp Leu Asp Gln Tyr Pro			
450	455	460	
Leu Gly Arg Lys Phe Leu Val Gln Ala Gly Leu Arg Arg Lys Pro Thr			
465	470	475	480
Ile Gly Pro Arg Lys Arg Ser Ala Pro Ser Ala Thr Thr Ser Ser Lys			
485	490	495	
Pro Ala Lys Arg Val Arg Val Ala Arg Lys			
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 gcagataaaa tattgcaatg gtcaagcctt ggtatatttt tgggtggact tggcataggt 180  
 actggaagtg gtacaggggg tcgtacaggg tacattccat tgggtggcg ttccaataca 240  
 gttgtggatg tcggctctac acgtcctcca gtggttattt aacctgtggg ccccacagac 300  
 ccatctatg ttacatata agaggactca agtgttgtt catcaggtgc acctaggcct 360  
 acttttactg gcacgtctgg gtttgatata acatctgtg gtacaactac acctgcagg 420  
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 gtagcaggc cccgcctta cagtagggcc taccaacaag tggctgtggc taaccctgag 720  
 tttcttacac gtccatccct ttaatttacc tatgacaacc cggcccttga gctgtggac 780  
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 35 40 45  
 Ser Leu Gly Ile Phe Leu Gly Gly Leu Gly Ile Gly Thr Gly Ser Gly  
 50 55 60  
 Thr Gly Gly Arg Thr Gly Tyr Ile Pro Leu Gly Gly Arg Ser Asn Thr  
 65 70 75 80  
 Val Val Asp Val Gly Pro Thr Arg Pro Pro Val Val Ile Glu Pro Val  
 85 90 95  
 Gly Pro Thr Asp Pro Ser Ile Val Thr Leu Ile Glu Asp Ser Ser Val  
 100 105 110  
 Val Thr Ser Gly Ala Pro Arg Pro Thr Phe Thr Gly Thr Ser Gly Phe  
 115 120 125  
 Asp Ile Thr Ser Ala Gly Thr Thr Pro Ala Val Leu Asp Ile Thr  
 130 135 140  
 Pro Ser Ser Thr Ser Val Ser Ile Ser Thr Thr Asn Phe Thr Asn Pro  
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 Ala Phe Ser Asp Pro Ser Ile Ile Glu Val Pro Gln Thr Gly Glu Val  
 165 170 175  
 Ser Gly Asn Val Phe Val Gly Thr Pro Thr Ser Gly Thr His Gly Tyr  
 180 185 190  
 Glu Glu Ile Pro Leu Gln Thr Phe Ala Ser Ser Gly Thr Gly Glu Glu  
 195 200 205  
 Pro Ile Ser Ser Thr Pro Leu Pro Thr Val Arg Arg Val Ala Gly Pro  
 210 215 220  
 Arg Leu Tyr Ser Arg Ala Tyr Gln Gln Val Ser Val Ala Asn Pro Glu  
 225 230 235 240  
 Phe Leu Thr Arg Pro Ser Ser Leu Ile Thr Tyr Asp Asn Pro Ala Phe  
 245 250 255  
 Glu Pro Val Asp Thr Thr Leu Thr Phe Glu Pro Arg Ser Asn Val Pro  
 260 265 270  
 Asp Ser Asp Phe Met Asp Ile Ile Arg Leu His Arg Pro Ala Leu Thr  
 275 280 285  
 Ser Arg Arg Gly Thr Val Arg Phe Ser Arg Leu Gly Gln Arg Ala Thr  
 290 295 300  
 Met Phe Thr Arg Ser Gly Thr Gln Ile Gly Ala Arg Val His Phe Tyr  
 305 310 315 320  
 His Asp Ile Ser Pro Ile Ala Pro Ser Pro Glu Tyr Ile Glu Leu Gln  
 325 330 335  
 Pro Leu Val Ser Ala Thr Glu Asp Asn Gly Leu Phe Asp Ile Tyr Ala  
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 Asp Asp Ile Asp Pro Ala Met Pro Val Pro Ser Arg Pro Thr Thr Ser  
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 370 375 380  
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 385 390 395 400  
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 405 410 415  
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